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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/845,335

DATE: 12/07/2001

TIME: 16:49:52

Input Set : N:\Crf3\RULE60\09845335.txt
Output Set: N:\CRF3\12072001\I845335.raw

3 <110> APPLICANT: CLOUGH, BARBARA
4 PREISER, PETER
5 WILSON, ROBERT
7 <120> TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
8 MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
9 EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
11 <130> FILE REFERENCE: N68837B GCW PJC DP
13 <140> CURRENT APPLICATION NUMBER: 09/845,335
14 <141> CURRENT FILING DATE: 2001-08-29
16 <150> PRIOR APPLICATION NUMBER: 09/140,466
17 <151> PRIOR FILING DATE: 1998-08-26
19 <150> PRIOR APPLICATION NUMBER: US 60/056,246
20 <151> PRIOR FILING DATE: 1997-08-28
22 <160> NUMBER OF SEQ ID NOS: 14
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1230
28 <212> TYPE: DNA
29 <213> ORGANISM: Plasmodium falciparum
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(1230)
35 <400> SEQUENCE: 1
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37 Met Asn Asn Lys Leu Phe Leu Arg Asn Lys Gln His Ile Asn Leu Gly
38 1 5 10 15
40 act ata ggg cat gta gat cat gga aaa act aca aca aca gct ata 96
41 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Thr Ala Ile
42 20 25 30
44 tct tat tta tta aat tta caa gga tta tca aaa aaa tat aat tat tca 144
45 Ser Tyr Leu Leu Asn Leu Gln Gly Leu Ser Lys Lys Tyr Asn Tyr Ser
46 35 40 45
48 gat att gat tca gct cca gaa gaa aaa ata aga ggt att aca ata aat 192
49 Asp Ile Asp Ser Ala Pro Glu Glu Lys Ile Arg Gly Ile Thr Ile Asn
50 50 55 60
52 aca aca cat att gaa tat gaa act tta aca aaa cat tgt gct cat ata 240
53 Thr Thr His Ile Glu Tyr Glu Thr Leu Thr Lys His Cys Ala His Ile
54 65 70 75 80
56 gat tgt cca gga cat tcc gat tat att aaa aat atg att ata gga gcc 288
57 Asp Cys Pro Gly His Ser Asp Tyr Ile Lys Asn Met Ile Ile Gly Ala
58 85 90 95
60 aca caa atg gat ata gca att tta gta ata tct ata ata gat ggt ata 336
61 Thr Gln Met Asp Ile Ala Ile Leu Val Ile Ser Ile Ile Asp Gly Ile
62 100 105 110
64 atg cct caa act tat gaa cat tta tta ata aaa caa ata ggt ata 384
65 Met Pro Gln Thr Tyr Glu His Leu Leu Ile Lys Gln Ile Gly Ile
66 115 120 125

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68	aaa	aat	ata	att	att	ttt	tta	aat	aaa	gaa	gat	tta	tgt	gat	gat	gtt	432
69	Lys	Asn	Ile	Ile	Phe	Leu	Asn	Lys	Glu	Asp	Leu	Cys	Asp	Asp	Val		
70	130				135							140					
72	gaa	tta	ata	gat	ttt	ata	aaa	tta	gaa	gta	aat	gaa	tta	ttt	att	aaa	480
73	Glu	Leu	Ile	Asp	Phe	Ile	Lys	Leu	Glu	Val	Asn	Glu	Leu	Leu	Ile	Lys	
74	145				150							155				160	
76	tat	aat	ttt	gat	tta	aat	tat	ata	cat	ata	tta	act	ggt	tca	gca	tta	528
77	Tyr	Asn	Phe	Asp	Leu	Asn	Tyr	Ile	His	Ile	Leu	Thr	Gly	Ser	Ala	Leu	
78	165				170							175					
80	aat	gta	ata	aat	ata	att	caa	aaa	aat	aag	gat	tat	gaa	tta	ata	aaa	576
81	Asn	Val	Ile	Asn	Ile	Ile	Gln	Lys	Asn	Lys	Asp	Tyr	Glu	Leu	Ile	Lys	
82	180				185							190					
84	tct	aat	att	tgg	ata	caa	aaa	tta	aat	tat	tta	att	caa	ata	att	gat	624
85	Ser	Asn	Ile	Trp	Ile	Gln	Lys	Leu	Asn	Asn	Leu	Ile	Gln	Ile	Ile	Asp	
86	195				200							205					
88	aat	att	ata	ata	cct	act	aga	aaa	att	aat	gat	tac	ttt	tta	atg	tca	672
89	Asn	Ile	Ile	Ile	Pro	Thr	Arg	Lys	Ile	Asn	Asp	Tyr	Phe	Leu	Met	Ser	
90	210				215							220					
92	ata	gaa	gat	gta	ttt	tct	ata	aca	ggt	aga	ggt	aca	gta	gta	aca	ggt	720
93	Ile	Glu	Asp	Val	Phe	Ser	Ile	Thr	Gly	Arg	Gly	Thr	Val	Val	Thr	Gly	
94	225				230							235				240	
96	aag	att	gaa	caa	gga	tgt	ata	aat	tta	aat	gat	gaa	att	gaa	att	tta	768
97	Lys	Ile	Glu	Gln	Gly	Cys	Ile	Asn	Leu	Asn	Asp	Glu	Ile	Glu	Ile	Leu	
98	245				250							255					
100	aaa	ttt	gaa	aaa	tca	tct	cct	aat	tta	aca	aca	gtt	ata	gga	tta	gaa	816
101	Lys	Phe	Glu	Lys	Ser	Ser	Pro	Asn	Leu	Thr	Thr	Val	Ile	Gly	Ile	Glu	
102	260				265							270					
104	atg	ttt	aaa	aaa	caa	tta	aca	caa	gca	caa	tcc	gga	gat	aat	gta	ggt	864
105	Met	Phe	Lys	Lys	Gln	Leu	Thr	Gln	Ala	Gln	Ser	Gly	Asp	Asn	Val	Gly	
106	275				280							285					
108	att	tta	tta	aga	aat	att	caa	aaa	aaa	gat	ata	aaa	aga	ggt	atg	att	912
109	Ile	Leu	Leu	Arg	Asn	Ile	Gln	Lys	Lys	Asp	Ile	Lys	Arg	Gly	Met	Ile	
110	290				295							300					
112	tta	gca	aca	cct	aat	aaa	tta	aaa	gta	tat	aag	tct	ttt	ata	gct	gaa	960
113	Leu	Ala	Thr	Pro	Asn	Lys	Leu	Lys	Val	Tyr	Lys	Ser	Phe	Ile	Ala	Glu	
114	305				310							315				320	
116	aca	tat	att	tta	act	aaa	gaa	gaa	ggt	ggt	cgt	cat	aaa	cct	ttt	aat	1008
117	Thr	Tyr	Ile	Leu	Thr	Lys	Glu	Glu	Gly	Arg	His	Lys	Pro	Phe	Asn		
118	325				330							335					
120	att	gga	tat	aaa	cct	caa	ttt	ttt	att	cgt	aca	gta	gat	gtt	act	gga	1056
121	Ile	Gly	Tyr	Lys	Pro	Gln	Phe	Phe	Ile	Arg	Thr	Val	Asp	Val	Thr	Gly	
122	340				345							350					
124	gaa	att	aaa	aat	ata	tat	tta	aat	gaa	aat	gta	caa	aaa	gta	gct	ata	1104
125	Glu	Ile	Lys	Asn	Ile	Tyr	Leu	Asn	Glu	Asn	Val	Gln	Lys	Val	Ala	Ile	
126	355				360							365					
128	cct	gga	gat	aaa	ata	aca	tta	cat	att	gaa	tta	aaa	cat	tat	ata	gtg	1152
129	Pro	Gly	Asp	Lys	Ile	Thr	Leu	His	Ile	Glu	Leu	Lys	His	Tyr	Ile	Val	
130	370				375							380					
132	ttg	aca	tta	aat	atg	aaa	ttt	tct	att	aga	gaa	gga	aaa	aca	ata		1200

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133 Leu Thr Leu Asn Met Lys Phe Ser Ile Arg Glu Gly Gly Lys Thr Ile
134 385 390 395 400
136 gga gca ggt att ata aca gaa ata aaa aat 1230
137 Gly Ala Gly Ile Ile Thr Glu Ile Lys Asn
138 405 410
141 <210> SEQ ID NO: 2
142 <211> LENGTH: 410
143 <212> TYPE: PRT
144 <213> ORGANISM: Plasmodium falciparum
146 <400> SEQUENCE: 2
147 Met Asn Asn Lys Leu Phe Leu Arg Asn Lys Gln His Ile Asn Leu Gly
148 1 5 10 15
150 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ile
151 20 25 30
153 Ser Tyr Leu Leu Asn Leu Gln Gly Leu Ser Lys Lys Tyr Asn Tyr Ser
154 35 40 45
156 Asp Ile Asp Ser Ala Pro Glu Glu Lys Ile Arg Gly Ile Thr Ile Asn
157 50 55 60
159 Thr Thr His Ile Glu Tyr Glu Thr Leu Thr Lys His Cys Ala His Ile
160 65 70 75 80
162 Asp Cys Pro Gly His Ser Asp Tyr Ile Lys Asn Met Ile Ile Gly Ala
163 85 90 95
165 Thr Gln Met Asp Ile Ala Ile Leu Val Ile Ser Ile Ile Asp Gly Ile
166 100 105 110
168 Met Pro Gln Thr Tyr Glu His Leu Leu Ile Lys Gln Ile Gly Ile
169 115 120 125
171 Lys Asn Ile Ile Ile Phe Leu Asn Lys Glu Asp Leu Cys Asp Asp Val
172 130 135 140
174 Glu Leu Ile Asp Phe Ile Lys Leu Glu Val Asn Glu Leu Leu Ile Lys
175 145 150 155 160
177 Tyr Asn Phe Asp Leu Asn Tyr Ile His Ile Leu Thr Gly Ser Ala Leu
178 165 170 175
180 Asn Val Ile Asn Ile Ile Gln Lys Asn Lys Asp Tyr Glu Leu Ile Lys
181 180 185 190
183 Ser Asn Ile Trp Ile Gln Lys Leu Asn Asn Leu Ile Gln Ile Ile Asp
184 195 200 205
186 Asn Ile Ile Ile Pro Thr Arg Lys Ile Asn Asp Tyr Phe Leu Met Ser
187 210 215 220
189 Ile Glu Asp Val Phe Ser Ile Thr Gly Arg Gly Thr Val Val Thr Gly
190 225 230 235 240
192 Lys Ile Glu Gln Gly Cys Ile Asn Leu Asn Asp Glu Ile Glu Ile Leu
193 245 250 255
195 Lys Phe Glu Lys Ser Ser Pro Asn Leu Thr Thr Val Ile Gly Leu Glu
196 260 265 270
198 Met Phe Lys Lys Gln Leu Thr Gln Ala Gln Ser Gly Asp Asn Val Gly
199 275 280 285
201 Ile Leu Leu Arg Asn Ile Gln Lys Lys Asp Ile Lys Arg Gly Met Ile
202 290 295 300
204 Leu Ala Thr Pro Asn Lys Leu Lys Val Tyr Lys Ser Phe Ile Ala Glu

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205 305 310 315 320
 207 Thr Tyr Ile Leu Thr Lys Glu Glu Gly Gly Arg His Lys Pro Phe Asn
 208 325 330 335
 210 Ile Gly Tyr Lys Pro Gln Phe Phe Ile Arg Thr Val Asp Val Thr Gly
 211 340 345 350
 213 Glu Ile Lys Asn Ile Tyr Leu Asn Glu Asn Val Gln Lys Val Ala Ile
 214 355 360 365
 216 Pro Gly Asp Lys Ile Thr Leu His Ile Glu Leu Lys His Tyr Ile Val
 217 370 375 380
 219 Leu Thr Leu Asn Met Lys Phe Ser Ile Arg Glu Gly Gly Lys Thr Ile
 220 385 390 395 400
 222 Gly Ala Gly Ile Ile Thr Glu Ile Lys Asn
 223 405 410
 227 <210> SEQ ID NO: 3
 228 <211> LENGTH: 409
 229 <212> TYPE: PRT
 230 <213> ORGANISM: Anacystis nidulans
 232 <400> SEQUENCE: 3
 233 Met Ala Arg Ala Lys Phe Glu Arg Thr Lys Pro His Ala Asn Ile Gly
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 236 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
 237 20 25 30
 239 Thr Thr Val Leu Ala Lys Ala Gly Met Ala Lys Ala Arg Ala Tyr Ala
 240 35 40 45
 242 Asp Ile Asp Ala Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
 243 50 55 60
 245 Thr Ala His Val Glu Tyr Glu Thr Gly His Arg His Tyr Ala His Val
 246 65 70 75 80
 248 Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
 249 85 90 95
 251 Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Ala Asp Gly Pro
 252 100 105 110
 254 Met Pro Gln Thr Arg Glu His Ile Leu Leu Ala Lys Gln Val Gly Val
 255 115 120 125
 257 Pro Asn Ile Val Val Phe Leu Asn Lys Glu Asp Met Val Asp Asp Ala
 258 130 135 140
 260 Glu Leu Leu Glu Leu Val Glu Leu Glu Val Arg Glu Leu Leu Ser Ser
 261 145 150 155 160
 263 Tyr Asp Phe Pro Gly Asp Asp Ile Pro Ile Val Ala Gly Ser Ala Leu
 264 165 170 175
 266 Gln Ala Leu Glu Ala Ile Gln Gly Gly Ala Ser Gly Gln Lys Gly Asp
 267 180 185 190
 269 Asn Pro Trp Val Asp Lys Ile Leu Lys Leu Met Glu Glu Val Asp Ala
 270 195 200 205
 272 Tyr Ile Pro Thr Pro Glu Arg Glu Val Asp Arg Pro Phe Leu Met Ala
 273 210 215 220
 275 Val Glu Asp Val Phe Thr Ile Thr Gly Arg Gly Thr Val Ala Thr Gly
 276 225 230 235 240
 278 Arg Ile Glu Arg Gly Ser Val Lys Val Gly Glu Thr Ile Glu Ile Val

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Input Set : N:\Crf3\RULE60\09845335.txt
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279	245	250	255	
281	Gly Leu Arg Asp Thr Arg Ser Thr Thr Val Thr Gly Val Glu Met Phe			
282	260	265	270	
284	Gln Lys Thr Leu Asp Glu Gly Leu Ala Gly Asp Asn Val Gly Leu Leu			
285	275	280	285	
287	Leu Arg Gly Ile Gln Lys Thr Asp Ile Glu Arg Gly Met Val Leu Ala			
288	290	295	300	
290	Lys Pro Gly Ser Ile Thr Pro His Thr Lys Phe Glu Ser Glu Val Tyr			
291	305	310	315	320
293	Val Leu Lys Lys Glu Glu Gly Gly Arg His Thr Pro Phe Phe Pro Gly			
294	325	330	335	
296	Tyr Arg Pro Gln Phe Tyr Val Arg Thr Thr Asp Val Thr Gly Ala Ile			
297	340	345	350	
299	Ser Asp Phe Thr Ala Asp Asp Gly Ser Ala Ala Glu Met Val Ile Pro			
300	355	360	365	
302	Gly Asp Arg Ile Lys Met Thr Val Glu Leu Ile Asn Pro Ile Ala Ile			
303	370	375	380	
305	Glu Gln Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile Gly			
306	385	390	395	400
308	Ala Gly Val Val Ser Lys Ile Leu Gln			
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314	<211> LENGTH: 408			
315	<212> TYPE: PRT			
316	<213> ORGANISM: Cryptomonas phi			
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322	Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile			
323	20	25	30	
325	Ser Ala Thr Leu Ser Gln Tyr Thr Gly Lys Ser Lys Lys Phe Asp Glu			
326	35	40	45	
328	Ile Asp Ser Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn Thr			
329	50	55	60	
331	Ala His Val Glu Tyr Glu Thr Asp Lys Trp Tyr Tyr Ala His Val Asp			
332	65	70	75	80
334	Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala Ala			
335	85	90	95	
337	Gln Met Asp Gly Ala Ile Leu Val Cys Ser Ala Ala Asn Gly Pro Met			
338	100	105	110	
340	Pro Gln Thr Arg Glu His Ile Leu Leu Ala Lys Gln Val Gly Val Pro			
341	115	120	125	
343	Tyr Ile Val Val Phe Leu Asn Lys Ala Asp Met Val Asp Asp Glu Glu			
344	130	135	140	
346	Leu Leu Glu Leu Val Gln Leu Glu Val Gln Glu Leu Leu Glu Lys Tyr			
347	145	150	155	160
349	Asp Phe Pro Gly Ser Glu Ile Pro Phe Val Ala Gly Ser Ala Leu Leu			
350	165	170	175	
352	Ala Leu Glu Ala Val Ala Asn Asn Pro Thr Ile Lys Arg Gly Glu Asp			

VERIFICATION SUMMARY

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